

Figure 1A

S. pneumoniae -----MKTRITELLKIDYPTFQCGMAWVADGDLGAVSKAGGLGIIGCGNAP.KEVVKANTDKIKSLTDKFFGVN
Ent. faecalis MKCTYLRTKGRIKSMNQELCELLGNYPTFQCGMAWVADASLASAVSNAGGLGIITAGGNAP.KEVVKKETKKVKELTECPFGVN
C. difficile -----MNKICKILNTKYPTFQCGMAWVATASLASAVSNAGGLGIITAGGNAP.KEALIKKELIVECKLTDKFFGVN
P. aeruginosa -----MGVFRTRFTETFGVEHPIMQCGMCWVGRAEEMAAAVANAGGLATLSALTQESPEALAAETIARCRELTDRFFGVN

IMML...SEFV.EDIIVDLVIEGVKVVITGAGNEFSKYMERFHEAGIIVIPVVSVALAKRMEKIGADAVIAEGMEAGGHIG...KLTTWTLVRQVATATS
 IMML...SEFA.DSIVDLVCEQVPVVITGAGNEAKYMARFKEHNKVIIPVVSVALAKRMEKIGADAVIFEGMEAGGHIG...KLTTWTLVRQVATATS
 VMLM...SEFV.DDIIDLIIEKVQVITGAGNEAKYMDRLKEAGTKVIIPVPTIALAQRMEKLGATAVIAEGTEGGGHIG...ELTTWTLVRQVADAVN
 LTLPTQKEVPYAEYRAAIIIEAGIRVVETACNDEGEHIAEFRRHGVKVIHKCTAVRHALLAERLGVDAVSIDGFEACAGHPGEDDIPGLVLPAAANRLR

FAD

IPVIAAGGIAIGEGAAAGFMLGABAVOVGTRFVVAKESNAHENYKEKILKARDIDITISAQHFGHVAIKNQLTRDFELAEDAFKQEDPDLEIFEQM
 IPVIAAGGIGDGRGMAAFMLGABAVQLGTRFLIAKCNVHEDYKQVVKARDLDAVITCQHFGEVRTLKNKLTAAQYNQLEKQELQKEVPDLEMFEKI
 IPVIAAGGIVDGRGLAASFALGASAVQVGTRFTCSSECSVHSNYKNLVKAKDRDIIVTGRSTGHEVRTLKNKLSKEFLKMEONGATPEE...LDKK
 VPIIASGGFADGRGLVAALALGADA INMCTRFIATRECPHFAVKAATRAADERSDILMRSRLNTARVARNALSQEVLAIE...ARGGAGYADIAALV

GAGALAKAVVHGVDGGSVMAGQIAGLVSKETAEETIKDYGAAGKIQEEASRWTGVVRND
 GQALRKAVVDGMDYGSVMAGQIAGLTKKEETACEIIDSIMSECKAIVHKMNQRWG-----
 GTGALRFATVDGDIKGSFMAQQAAMVKEITCKELIEAMVNQAREIMPAIEL-----
 SGQRGRQVYQGGTDLGSIWSAGMVOGLIDDEPAEELLRDIVEQARQLVRQRLEGMLAGV---

Figure 1B

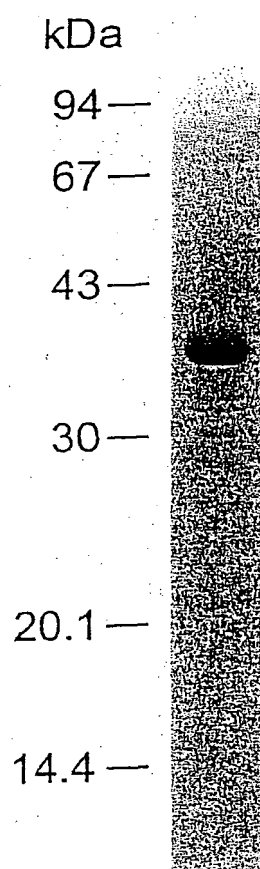


Figure 2A

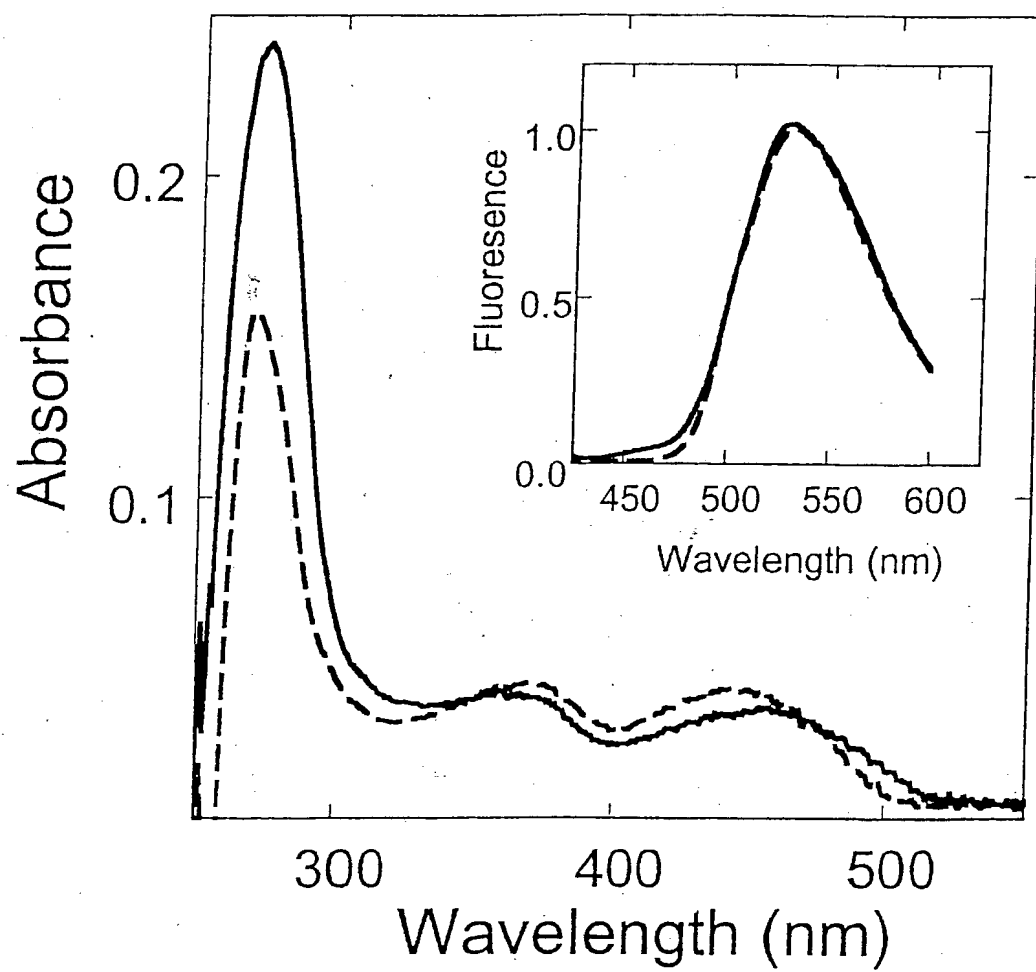


Figure 2B

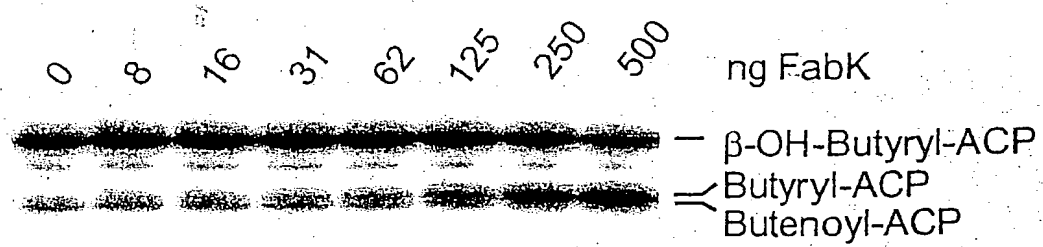


Figure 2C

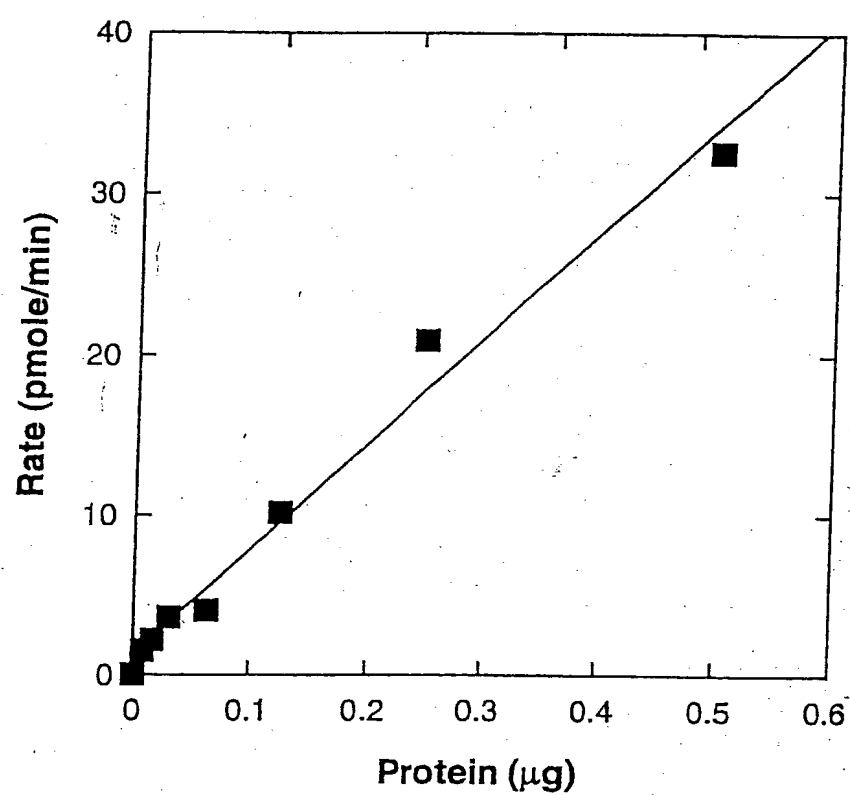


Figure 2D

FABL_BACSU ----MEQNKCALVTSSRGVCKAAATRLA..ENGYNTIVINVARSKKAALETAEEIE.KLGVKVLVVKANVGQPAKIKENFOQIDET
 FABL_HPYLO MNGSNHMKNTLVISGATRGIGKAIIFVRFA..QSGVNIAFTYNKNVEEANKIIEDVEQKYSIKAKAYSLNVLEPEQYTELFKQIDAD
 FABL_ECOLI ---MGFLSGKRILVTGVASKLSIAYGLAQAMHREGAELAFYQNDKLGCR..VEEFAAQLGSDI.VLQCDVAEDASIDTMEAEELGKV

FGRLLDVFNN.A.....ASGVLRPVMEEETHNDWTMNAKALFCAQEAAKLMEKNGGCHIVSISLCSIRYLENYTTVCVSKAALEALTRYLAVE
 FDRVDFEISN.AITYGRSVVGGFAPFMRLKPKGLNNIYTATVLAHVGAQEAAKRMOKTGGCAIVSLSTCNLVVMPNYAGHCNSKNNAVETMVKYAAMD
 WPKFDGFSVHSIGFAPGDQLDGDY..VNAVTRREGFKIARDISSYSFVAMAKACRSMI..NPGSALLTLSYLGAERATPNYNVMGLAKASLEANNVRYMANA

LSPKQITVNAVSGGAIIDTDLKHFNRREDILEDARQNTFAGSMVEIKDMVDIVVEFLV.SSKADMIRGCTTIVDGGCSLLV-----
 LGEFNIRVNAVSGGPIIDTDLKAFPDYVEHKEKVEECSEPLKRMGNPNDLAGAAYFLCDETCSGWLTCGTTIVVDGGCTTFK-----
 MGPEGRVNAISAGPIRTLAASGIKDFRKM LAHCEAVTEIRRTVTIEDVGNAAFLCSDLSAG.ISGEVVHVDDGGFSLAAMNELELK

Figure 3